

FIG. 1A

tacacggccg cagctgaaca gcatcaccgc tgtcccaagg acaaccccaa agaggggcct 60  
cgactgcacc tcctcgaagt tgctggctgg ctttggcaag tgcaggaatg gtgttttgtg 120  
agggcatgga tggagaagtg ccaagggccc ctgttttggtc acttccgaag agcaaaaacg 180  
tgttgagagg agaccggttt aagatttcaa acagaacctc cccagcgcg c atgaaaggac 240  
ttgattagca tatgtcaaga ggacccgctt atatactcgg tgtgtatgta cacaggactc 300  
tgatctgac agtttgcgga attggagccc cagccaacag ccctagtcct agtattggca 360  
gcggcagcta tagatatttc tgcagagcca gcagccggct cccacctacc caaggagaga 420  
agatcgctcc aagacagtga gagcttcct gccatttcag tgcaaagtcc ctccggagcg 480  
acctcagagg agtaaccggg ccttaacttt ttgcgctcgt tttgctataa tttttctcta 540  
tccacctcca tcccaccccc acaacactct ttactggggg ggtcttttgt gttccggatc 600  
tccccctcc atg gct ccc tta gcc gaa gtc ggg ggc ttt ctg ggc ggc ctg 651  
Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu  
1 5 10  
gag ggc ttg ggc cag cag gtg ggt tgc cat ttc ctg ttg cct cct gcc 699  
Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala  
15 20 25 30  
ggg gag cgg ccg ccg ctg ctg ggc gag cgc agg agc gcg gcg gag cgg 747  
Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg  
35 40 45  
agc gcc cgc ggc ggc ccg ggg gct gcg cag ctg gcg cac ctg cac ggc 795  
Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly  
50 55 60  
atc ctg cgc cgc cgg cag ctc tat tgc cgc acc ggc ttc cac ctg cag 843  
Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln  
65 70 75  
atc ctg ccc gac ggc agc gtg cag ggc acc cgg cag gac cac agc ctc 891  
Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu  
80 85 90  
ttc ggt atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att 939  
Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile  
95 100 105 110  
aga ggt gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa 987  
Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu  
115 120 125

FIG. 1B

ctc tat gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag	1035
Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln	
130 135 140	
ttt gaa gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat	1083
Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His	
145 150 155	
gga gac act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act	1131
Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr	
160 165 170	
cca aga gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc	1179
Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe	
175 180 185 190	
tta cct aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag gac	1227
Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp	
195 200 205	
cta ctg atg tac act tga agtgcgatag tgacattatg gaagagtcaa	1275
Leu Leu Met Tyr Thr	
210	
accacaacca ttctttcttg tcatagttcc catcataaaaa taatgaccca agcag	1330

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FIG. 2

1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSA.R 49  
 |||| ||| : | : . | . .|| : || : : |  
 1 MAPLGEVGNVFGVQDAV..PFGNVPLPV..DSPVLLSDHLGQSEAGGLP 46  
 50 GGPGAAQLAHLHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSFLFGILE 99  
 || | || ||||| ||||| : | | . : ||| . ||| |||||  
 47 RGPVAVTDLHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILE 96  
 100 FISVAVGLVSIRGVDSGLYLG MNDKGELYGSEKLTSECIFREQFEENWYN 149  
 ||| : ||||| ||||| : ||||| ||| ||| |||||  
 97 FISIAVGLVSIRGVDSGLYLG MNEKGELYGSEKLTQECVFREQFEENWYN 146  
 150 TYSSNIYKHGDTGRRYFVALNKDGTPRDGARSKRHQKFTHFLPRPVDPER 199  
 ||||| : ||| ||||| : ||||| ||| : | . ||||| ||||| ||||| : :  
 147 TYSSNLYKHVDTGRRYYVALNKDGTREGTRTKRHQKFTHFLPRPVD PDK 196  
 200 VPELYKD LLMYT 211  
 ||||| : | .  
 197 VPELYKDILSQS 208

FIG. 3

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1 MAPLAEVGGFLGGLEGLGQQVGSFHLLPPAGERPPLLGERRSAAERSA.R 49
  |||| ||| : | : . |. .|| : || : .|
1 MAPLGEVGSYFGVQDAV..PFGNVPVLPV..DSPVLLSDHLGQSEAGGLP 46

50 GGPGAAQLAHLHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSFLFGILE 99
  || | || ||||| ||||| :| |. : |||. ||| |||||
47 RGPVAVTDLHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILE 96

100 FISVAVGLVSIRGVDSGLYLGMNDKGELYGSEKLTSECI FREQFEENWYN 149
  ||| : ||||| ||||| : ||||| ||||| ||| : ||||| |||||
97 FISIAVGLVSIRGVDSGLYLGMNEKGELYGSEKLTQECV FREQFEENWYN 146

150 TYSSNIYKHGDTGRRYFVALNKDGTPRDGARSKRHQKFTHFLPRPVDPER 199
  ||||| : ||| ||||| : ||||| ||||| :| |. ||||| ||||| ||||| : :
147 TYSSNLYKHVDTGRRYYVALNKDGTREGTRTKRHQKFTHFLPRPVD PDK 196

200 VPELYKDLLMYT 211
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197 VPELYKDILSQS 208

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FIG. 4

hu FGF-9	MAPLGEVGNV	FGVQDAV..P	FGNVPLPV.	.DSPVLLSDH	LQSEAGGLP	RGPAVTDLDH
hu FGF-16	MA...EVGGV	FASLDWDLHG	FSSSLGNVPL	ADSPGFLNER	LQIE.GKLQ	RGSP.TDFAH
hu FGF-L	MAPLAEVGGF	LGGLEGLGQQ	VGSHFLLPPA	GERPPLLGER	RSAAERSA.R	GGPGAAQLAH
mu FGF-9	MAPLGEVGSY	FGVQDAV..P	FGNVPLPV.	.DSPVLLNDH	LQSEAGGLP	RGPAVTDLDH
ra FGF-16	MA...EVGGV	FASLDWDLQG	FSSSLGNVPL	ADSPGFLNER	LQIE.GKLQ	RGSP.TDFAH
hu FGF-9	LKGILRRRQL	YCRTGFHLEI	FPNGTIQGTR	KDHSRFGILE	FISIAVGLVS	IRGVDSGLYL
hu FGF-16	LKGILRRRQL	YCRTGFHLEI	FPNGTVHGTR	HDHSRFGILE	FISLAVGLIS	IRGVDSGLYL
hu FGF-L	LHGILRRRQL	YCRTGFHLQI	LPDGSVQGTR	QDHSLFGILE	FISVAVGLVS	IRGVDSGLYL
mu FGF-9	LKGILRRRQL	YCRTGFHLEI	FPNGTIQGTR	KDHSRFGILE	FISIAVGLVS	IRGVDSGLYL
ra FGF-16	LKGILRRRQL	YCRTGFHLEI	FPNGTVHGTR	HDHSRFGILE	FISLAVGLIS	IRGVDSGLYL
hu FGF-9	GMNEKGELYG	SEKLTQECVF	REQFEENWYN	TYSSNLYKHV	DTGRRYYVAL	NKDGTTPREGT
hu FGF-16	GMNERGELYG	SKKLTRECVF	REQFEENWYN	TYASTLYKHS	DSERQYYVAL	NKDGSPPREGY
hu FGF-L	GMNDKGELYG	SEKLTSECIF	REQFEENWYN	TYSSNIYKHG	DTGRRYFVAL	NKDGTTPRDGA
mu FGF-9	GMNEKGELYG	SEKLTQECVF	REQFEENWYN	TYSSNLYKHV	DTGRRYYVAL	NKDGTTPREGT
ra FGF-16	GMNERGELFG	SKKLTRECVF	REQFEENWYN	TYASTLYKHS	DSERQYYVAL	NKDGSPPREGY
hu FGF-9	RTKRHHQKFTH	FLPRPVDPPDK	VPELYKDILS	QS		
hu FGF-16	RTKRHHQKFTH	FLPRPVDPSK	LPSMSRDLFH	YR		
hu FGF-L	RSKRHHQKFTH	FLPRPVDPER	VPELYKDILM	YT		
mu FGF-9	RTKRHHQKFTH	FLPRPVDPPDK	VPELYKDILS	QS		
ra FGF-16	RTKRHHQKFTH	FLPRPVDPSK	LPSMSRDLFR	YR		